

Om protein - protein search, using Bw model									
Run on: July 13, 2004, 12:50:24 ; Search time 14.5 Seconds									
(without alignments)									
53.406 Million cell updates/sec									
Title: US-09-830-839-1									
Title: Perfect score: 79	Sequence: 1 MTEQQWNFAGIEAA	15							
Scoring table: BLOSUM62	Gappp 10.0 , Gapext 0.5								
Searched: 389414 seqs, 51625971 residues									
Total number of hits satisfying chosen parameters: 389414									
Minimum DB seq length: 0									
Maximum DB seq length: 200000000									
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries									
Database : Issued_Patents_AA:*									
1: /cgns2_6/podata/2/iaa/5A_COMB.pep:*									
2: /cgns2_6/podata/2/iaa/5B_COMB.pep:*									
3: /cgns2_6/podata/2/iaa/6A_COMB.pep:*									
4: /cgns2_6/podata/2/iaa/6B_COMB.pep:*									
5: /cgns2_6/podata/2/iaa/PCITS_COMB.pep:*									
6: /cgns2_6/podata/2/iaa/backfilest1.pep:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	% Query	Match Length	DB ID	Description	RESULT 1	US-09-818-112-104	Sequence 104, Application US/08818112	ALIGNMENTS
1	79	100.0	51	3	US-09-818-112-104	GENERAL INFORMATION:			
2	79	100.0	51	4	US-09-818-111-99	PATENT NO. 6290969			
3	79	100.0	51	4	US-09-556-556-104	APPLICANT: Reed, Steven G.			
4	79	100.0	51	4	US-09-072-596-99	APPLICANT: Steiky, Yasir A.W.			
5	79	100.0	51	4	US-09-072-596-104	APPLICANT: Dillon, Davin C.			
6	79	100.0	95	2	US-09-655-640-2	APPLICANT: Campos-Meto, Antonio			
7	79	100.0	403	4	US-09-050-739-173	APPLICANT: Houghton, Raymond			
8	79	100.0	404	4	US-09-050-739-172	APPLICANT: Vedwick, Thomas S.			
9	52	65.3	10	3	US-09-001-984C-77	APPLICANT: Twardzik, Daniel R.			
10	52	65.8	10	4	US-09-96-347F-77	TITLE OF INVENTION: COMPOUNDS AND METHODS FOR			
11	42	53.2	409	4	US-09-98-432A-554	TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS			
12	42	53.2	413	1	US-09-579-667-4	NUMBER OF SEQUENCES: 153			
13	41	51.9	176	4	US-09-162-842-3	CORRESPONDENCE ADDRESS:			
14	41	51.9	176	4	US-09-193-171-3	ADDRESSEE: SEED and BERRY LLP			
15	39	49.4	538	4	US-09-252-991A-18026	STREET: 6300 Columbia Center, 701 Fifth Avenue			
16	39	49.4	928	4	US-09-352-991A-24200	STATE: Seattle			
17	38	48.1	155	3	US-08-885-888-3	CITY: Seattle			
18	38	48.1	155	3	US-08-505-880C-3	STATE: Washington			
19	38	48.1	349	4	US-09-189-039A-13578	COUNTRY: USA			
20	38	48.1	410	1	US-08-679-667-2	ZIP: 98103-7092			
21	38	48.1	410	1	US-08-579-667-6	COMPUTER READABLE FORM:			
22	38	48.1	410	1	US-08-579-667-8	MEDIUM TYPE: Floppy disk			
23	38	48.1	795	4	US-09-552-991A-36635	COMPILER: IBM PC compatible			
24	38	48.1	2293	3	US-09-368-550-2	OPERATING SYSTEM: PC-DOS/MS-DOS			
25	37	46.8	331	4	US-09-489-039A-9639	SOFTWARE: Patent in Release #1.0, Version #1.			
26	37	46.8	435	4	US-09-252-991A-21220	CURRENT APPLICATION DATA:			
27	37	46.8	493	4	US-09-540-236-2120	APPLICATION NUMBER: US/08/818, 112			
						FILING DATE: 13-MAR-1997			
						CLASSIFICATION: 424			
						ATTORNEY/AGENT INFORMATION:			
						NAME: Maki, David J.			
						REGISTRATION NUMBER: 31,392			
						REFERENCE/DOCKET NUMBER: 210121.411C6			
						TELECOMMUNICATION INFORMATION:			
						TELEPHONE: (206) 682-6031			
						TELEFAX: (206) 682-6031			
						INFORMATION FOR SEQ ID NO: 104:			
						SEQUENCE CHARACTERISTICS:			
						LENGTH: 51 amino acids			
						TYPE: amino acid			
						STRANDEDNESS: single			
						TOPOLOGY: linear			
						US-08-818-112-104			
						Query Match	100.0%	Score 79;	DB 3;
						Best Local Similarity	100.0%	Pred. No. 4.1e-07	
						Matches	15;	Conservative 0;	Mismatches 0

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Sequence 6437, Ap
Sequence 80, Appl
Sequence 265, App
Sequence 8963, Ap
Sequence 115, App
Sequence 113, App
Sequence 4, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 15, Appl
Sequence 8, Appl
Sequence 18, Appl
Sequence 36, Appl
Sequence 28, Appl
Sequence 4, Appl
Sequence 5645, Ap

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## OM protein - protein search, using sw model

Run on: July 13, 2004, 12:54:00 ; Search time 40 Seconds  
(without alignments)

116.969 Million cell updates/sec

Title: US-09-830-839-1

Perfect score: 79

Sequence: 1 MTBQQWINPAGIERRA 15

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters:

1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA: \*

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1: /cgn2_6/ptodata/1/pubpa/PICTUS_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB_pep:*
4: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB_pep:*
5: /cgn2_6/ptodata/1/pubpa/US07_NEW_PUB_pep:*
6: /cgn2_6/ptodata/1/pubpa/PICTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB_pep:*
8: /cgn2_6/ptodata/1/pubpa/PUBCOMB_pep:*
9: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB_pep:*
10: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB_pep:*
11: /cgn2_6/ptodata/1/pubpa/US09_PUBCOMB_pep:*
12: /cgn2_6/ptodata/1/pubpa/US09_NEW_PUB_pep:*
13: /cgn2_6/ptodata/1/pubpa/PUBCOMB_pep:*
14: /cgn2_6/ptodata/1/pubpa/US10_PUBCOMB_pep:*
15: /cgn2_6/ptodata/1/pubpa/US10_NEW_PUB_pep:*
16: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB_pep:*
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18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB_pep:*
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**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	79	100.0	15	14	US-10-079-167-79
2	79	100.0	15	15	US-10-079-167-79
3	79	100.0	51	12	US-09-885-3491-33
4	79	100.0	51	14	US-10-193-002-99
5	79	100.0	51	14	US-10-084-841-104
6	79	100.0	51	14	US-10-098-7318-33
7	79	100.0	95	9	US-09-805-4274-1
8	79	100.0	95	11	US-09-875-503-1
9	79	100.0	403	9	US-09-791-171-173
10	79	100.0	403	9	US-09-805-4274-4
11	79	100.0	403	10	US-09-804-980-173
12	79	100.0	403	11	US-09-872-503-4
13	79	100.0	403	12	US-09-943-413-173
14	79	100.0	403	16	US-10-620-241-173
15	100.0		404	9	US-09-791-171-172

## ALIGNMENTS

```

RESULT 1
US-10-079-167-79
; Sequence 79, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; CURRENT APPLICATION NUMBER: US/10079167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1995-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 79
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE: OTHER INFORMATION: T cell epitope in ESAT6
; OTHER INFORMATION: T cell epitope in ESAT6
US-10-079-167-79
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Query Match 100.0%; Score 79; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## Om protein - protein search, using SW model

Run on: July 13, 2004, 12:50:24 ; Search time 14.5 Seconds  
(without alignments)  
53.406 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIERRASAIAQG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:

- 1: /cgn2\_6/prodata/2/iaa/5A\_COMB\_pep:\*
- 2: /cgn2\_6/prodata/2/iaa/5B\_COMB\_pep:\*
- 3: /cgn2\_6/prodata/2/iaa/6A\_COMB\_pep:\*
- 4: /cgn2\_6/prodata/2/iaa/6B\_COMB\_pep:\*
- 5: /cgn2\_6/prodata/2/iaa/PC705\_COMB\_pep:\*
- 6: /cgn2\_6/prodata/2/iaa/backfile1.pop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Length DB ID Description

Result No.	Score	Query	Length	DB	ID	Description
1	77	100.0	51	3	US-09-818-112-104	Sequence 104, App
2	77	100.0	51	4	US-09-818-111-99	Sequence 99, App
3	77	100.0	51	4	US-09-818-111-99	Sequence 104, App
4	77	100.0	51	4	US-09-072-556-104	Sequence 99, App
5	77	100.0	51	4	US-09-072-556-104	Sequence 104, App
6	77	100.0	95	2	US-09-072-967-104	Sequence 2, Appl.
7	77	100.0	403	4	US-09-050-739-173	Sequence 173, App
8	77	100.0	404	4	US-09-050-739-172	Sequence 172, App
9	42.5	50.6	404	4	US-09-050-739-173	Sequence 173, App
10	42	54.5	409	4	US-09-252-991A-29788	Sequence 554, App
11	41	53.2	149	4	US-09-252-991A-29788	Sequence 265, App
12	41	53.2	282	4	US-09-634-218-265	Sequence 113, App
13	40	51.9	2293	3	US-09-368-501-2	Sequence 2, Appl.
14	39	50.6	221	4	US-09-904-615-155	Sequence 155, App
15	39	50.6	413	4	US-09-252-991A-29788	Sequence 2978, App
16	39	50.6	1138	4	US-09-489-039A-13574	Sequence 13574, App
17	38	49.4	185	4	US-09-489-039A-13336	Sequence 11336, App
18	38	49.4	349	4	US-09-489-039A-13578	Sequence 13578, App
19	38	49.4	365	4	US-09-252-991A-30166	Sequence 30166, App
20	38	49.4	418	4	US-09-028-813B-4	Sequence 4, Appl.
21	38	49.4	435	4	US-09-252-991A-23220	Sequence 23220, App
22	37	48.1	209	4	US-09-252-991A-24013	Sequence 24013, App
23	37	48.1	360	4	US-09-509-902A-9	Sequence 9, Appl.
24	37	47.5	475	4	US-09-252-991A-20838	Sequence 20838, App
25	37	48.1	947	4	US-09-252-991A-21335	Sequence 21335, App
26	37	48.1	1138	4	US-09-252-991A-23952	Sequence 25952, App
27	36	46.8	294	4	US-09-489-039A-10933	Sequence 10933, App

## ALIGNMENTS

RESULT 1	US-09-818-112-104	Sequence 13907, A
	; Sequence 104, Application US/08818112	Sequence 10986, A
	; Patent No. 6290969	Sequence 13753, A
	GENERAL INFORMATION:	Sequence 8540, App
	APPLICANT: Reed, Steven G.	Sequence 3817, App
	APPLICANT: Sheiky, Yasir A.W.	Sequence 74, App
	APPLICANT: Dillon, Davin C.	Sequence 11, App
	APPLICANT: Campos-Neto, Antonio	Sequence 74, App
	APPLICANT: Houghton, Raymond	Sequence 3, App
	APPLICANT: Vecvick, Thomas S.	Sequence 232, App
	APPLICANT: Twardzik, Daniel R.	Sequence 80, App
	TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY	Sequence 18, App
	NUMBER OF SEQUENCES: 153	
	CORRESPONDENCE ADDRESS:	
	STREET: 6390 Columbia Center, 701 Fifth Avenue	
	CITY: Seattle	
	STATE: Washington	
	COUNTRY: USA	
	ZIP: 98104-7092	
	COMPILER READABLE FORM:	
	MEDIUM TYPE: FLOPPY disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: PatentIn Release #1.0, Version #1.30	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/09/818,112	
	FILING DATE: 11-MAR-1997	
	CLASSIFICATION: 424	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Maki, David J.	
	REGISTRATION NUMBER: 31,392	
	REFERENCE/DOCKET NUMBER: 210121.411C6	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (206) 622-4900	
	TELEFAX: (206) 682-6031	
	INFORMATION FOR SEQ ID NO: 104:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 51 amino acids	
	TYPE: amino acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	

Query Match 100.0%; Score 77; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06; Indels 0; Gaps 0;

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Gencore - version 5.1.6

On protein - protein search, using sw model

Run on:

July 13, 2004, 12:54:00 ; Search time 40 Seconds

(without alignments)

115.969 Million cell updates/sec

Title: US-09-830-839-6

Perfect score: 77

Sequence: 1 WNFAGIEAAASAIQG 15

Scoring table: BLASTm62

Gapext 10.0 , Gapext 0.5

Searched:

1279676 seqs, 311919243 residues

Total number of hits satisfying chosen parameters:

1279676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:  
 1: /cggn2\_6/prodata/1/pubpa/PCTUS\_PUBCOMB.pep: \*  
 2: /cggn2\_6/prodata/1/pubpa/US07\_PUBCOMB.pep: \*  
 3: /cggn2\_6/prodata/1/pubpa/US06\_PUBCOMB.pep: \*  
 4: /cggn2\_6/prodata/1/pubpa/US05\_PUBCOMB.pep: \*  
 5: /cggn2\_6/prodata/1/pubpa/US07\_NEW\_PUBCOMB.pep: \*  
 6: /cggn2\_6/prodata/1/pubpa/US08\_PUBCOMB.pep: \*  
 7: /cggn2\_6/prodata/1/pubpa/US09\_PUBCOMB.pep: \*  
 8: /cggn2\_6/prodata/1/pubpa/US09A\_PUBCOMB.pep: \*  
 9: /cggn2\_6/prodata/1/pubpa/US09B\_PUBCOMB.pep: \*  
 10: /cggn2\_6/prodata/1/pubpa/US09C\_PUBCOMB.pep: \*  
 11: /cggn2\_6/prodata/1/pubpa/US09D\_PUBCOMB.pep: \*  
 12: /cggn2\_6/prodata/1/pubpa/US09\_ENEW\_PUBCOMB.pep: \*  
 13: /cggn2\_6/prodata/1/pubpa/US10A\_PUBCOMB.pep: \*  
 14: /cggn2\_6/prodata/1/pubpa/US10B\_PUBCOMB.pep: \*  
 15: /cggn2\_6/prodata/1/pubpa/US10C\_PUBCOMB.pep: \*  
 16: /cggn2\_6/prodata/1/pubpa/US10\_ENEW\_PUBCOMB.pep: \*  
 17: /cggn2\_6/prodata/1/pubpa/US60\_NEWPUBCOMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	77	100.0	15 14 US-10-079-167-80	Sequence 80, Appl
2	77	100.0	15 15 US-10-345-000-2	Sequence 60, Appl
3	77	100.0	20 9 US-09-813-333-60	Sequence 60, Appl
4	77	100.0	20 12 US-10-239-103-60	Sequence 60, Appl
5	77	100.0	20 13 US-10-044-703-60	Sequence 60, Appl
6	77	100.0	51 12 US-09-886-349A-33	Sequence 33, Appl
7	77	100.0	51 14 US-10-193-002-99	Sequence 99, Appl
8	77	100.0	51 14 US-10-084-843-104	Sequence 104, Appl
9	77	100.0	51 14 US-10-098-732A-33	Sequence 33, Appl
10	77	100.0	95 9 US-09-805-427A-1	Sequence 1, Appl
11	77	100.0	95 11 US-09-872-505-1	Sequence 1, Appl
12	77	100.0	403 9 US-09-791-171-173	Sequence 173, Appl
13	77	100.0	403 9 US-09-805-427A-4	Sequence 4, Appl
14	77	100.0	403 10 US-09-804-980-173	Sequence 4, Appl
15	77	100.0	US-09-872-505-173	Sequence 4, Appl
16	77	100.0	403 12 US-09-943-443-173	Sequence 173, App
17	77	100.0	403 16 US-10-620-246-173	Sequence 172, App
18	77	100.0	404 9 US-09-805-427A-3	Sequence 3, Appl
19	77	100.0	404 10 US-09-804-980-172	Sequence 172, App
20	77	100.0	404 11 US-09-872-505-3	Sequence 3, Appl
21	77	100.0	404 12 US-09-943-443-172	Sequence 172, App
22	77	100.0	404 16 US-10-620-246-172	Sequence 172, App
23	77	100.0	404 9 US-09-813-333-61	Sequence 61, Appl
24	66	85.7	20 12 US-10-239-103-61	Sequence 61, Appl
25	66	85.7	20 13 US-10-044-703-61	Sequence 61, Appl
26	66	85.7	20 15 US-10-344-000-1	Sequence 61, Appl
27	60	77.9	13 9 US-09-813-333-59	Sequence 59, Appl
28	60	77.9	13 12 US-10-239-103-59	Sequence 59, Appl
29	60	77.9	13 13 US-09-813-333-59	Sequence 59, Appl
30	54	70.1	15 14 US-10-079-167-79	Sequence 79, Appl
31	54	70.1	15 15 US-10-344-000-1	Sequence 79, Appl
32	43	55.8	400 15 US-369-493-21850	Sequence 21850, A
33	42.5	55.2	141 12 US-10-389-647-560	Sequence 560, App
34	42	54.5	409 15 US-10-289-762-554	Sequence 554, App
35	42	54.5	1447 16 US-10-431-963-133273	Sequence 133273, Sequence 108079,
36	41	53.2	149 16 US-10-437-961-108079	Sequence 168, APP
37	41	53.2	149 15 US-10-264-213-168	Sequence 113, APP
38	41	53.2	282 14 US-10-288-930-113	Sequence 908, AP
39	41	53.2	443 15 US-10-369-493-9058	Sequence 76999, A
40	41	53.2	445 12 US-10-282-122A-76999	Sequence 12053, A
41	41	53.2	463 14 463 14 US-10-156-761-12653	Sequence 50764, A
42	41	53.2	528 12 US-10-282-122A-50754	Sequence 69721, A
43	41	53.2	893 12 US-10-282-122A-69721	Sequence 165952, Sequence 164110,
44	40	51.9	419 16 US-10-437-963-164110	Sequence 164110,
45	40	51.9	934 16 US-10-437-963-164110	Sequence 164110,

#### ALIGNMENTS

RESULT 1  
 US-10-079-167-80  
 ; Sequence 80, Application US/10079167

; Publication No. US2003013454A1  
 ; GENERAL INFORMATION:

; APPLICANT: Hill, Adrian V.S.

; APPLICANT: McShane, Helen

; APPLICANT: Gilbert, Sarah C.

; APPLICANT: Reece, William

; APPLICANT: Schneider, Joerg

; TITLE OF INVENTION: Vaccination Method

; FILE REFERENCE: 2907-1000-001

; CURRENT APPLICATION NUMBER: US10/079,157

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: US 09/454,204

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: PCT/GB98/01681

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: PCT/GB01/04116

; PRIOR FILING DATE: 2001-09-13

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastaSQ for Windows Version 4.0

; SEQ ID NO: 80

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE: OTHER INFORMATION: T cell epitope in ESAT6

; US-10-079-167-80

; Query Match 100.0%; Score 77; DB 14; Length 15;

; Best Local Similarity 100.0%; Pred. No. 2e-06%; Mismatches 15; Conservative 0%; Indels 0; Gaps 0;